

PCT09

## RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/830,762

TIME: 14:11:04

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\11142001\I830762.raw

3 <110> APPLICANT: Shipp, Margaret  
4 Aguiar, Ricardo  
5 Yakushijin, Yoshi  
7 <120> TITLE OF INVENTION: LYMPHOMA ASSOCIATED MOLECULES AND USES THEREFOR  
9 <130> FILE REFERENCE: DFN-031US  
11 <140> CURRENT APPLICATION NUMBER: US 09/830,762  
12 <141> CURRENT FILING DATE: 2001-04-27  
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/25439  
16 <151> PRIOR FILING DATE: 1999-10-29  
18 <150> PRIOR APPLICATION NUMBER: US 60/106,383  
19 <151> PRIOR FILING DATE: 1998-10-29  
21 <150> PRIOR APPLICATION NUMBER: US 60/106,448  
22 <151> PRIOR FILING DATE: 1998-10-30  
24 <160> NUMBER OF SEQ ID NOS: 6  
26 <170> SOFTWARE: PatentIn Ver. 2.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 3243  
30 <212> TYPE: DNA  
31 <213> ORGANISM: Homo sapiens  
33 <220> FEATURE:  
34 <221> NAME/KEY: CDS  
35 <222> LOCATION: (229)..(2790)  
37 <400> SEQUENCE: 1

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40 ggaagtagct ctccagcttc ctctgtactc gggggccgga ctgtacacc cgcacgagga 120  
42 gcggggacgg cgggcgcgaga agtggggccac catatctgga aactacagtc tatgctttga 180  
44 agcgcaaaag ggaataaaca tttaaagact ccccggggga cctggagg atg gac ttt 237  
45 Met Asp Phe  
46 1

48 tcc atg gtg gcc gga gca gca gct tac aat gaa aaa tca ggt agg att 285  
49 Ser Met Val Ala Gly Ala Ala Ala Tyr Asn Glu Lys Ser Gly Arg Ile  
50 5 10 15  
52 acc tcg ctc tca ctc ttg ttt cag aaa gtc ttt gct cag atc ttt cct 333  
53 Thr Ser Leu Ser Leu Leu Phe Gln Lys Val Phe Ala Gln Ile Phe Pro  
54 20 25 30 35  
56 cag tgg aga aag ggg aat aca gaa gaa tgt ctc ccc tac aag tgc tca 381  
57 Gln Trp Arg Lys Gly Asn Thr Glu Glu Cys Leu Pro Tyr Lys Cys Ser  
58 40 45 50  
60 gag act ggt gct ctt gga gaa aac tat agt tgg caa att ccc att aac 429  
61 Glu Thr Gly Ala Leu Gly Glu Asn Tyr Ser Trp Gln Ile Pro Ile Asn  
62 55 60 65  
64 cac aat gac ttc aaa att tta aaa aat aat gag cgt cag ctg tgt gaa 477  
65 His Asn Asp Phe Lys Ile Leu Lys Asn Asn Glu Arg Gln Leu Cys Glu  
66 70 75 80  
68 gtc ctc cag aat aag ttt ggc tgt atc tct acc ctg gtc tct cca gtt 525  
69 Val Leu Gln Asn Lys Phe Gly Cys Ile Ser Thr Leu Val Ser Pro Val  
70 85 90 95

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72 cag gaa ggc aac agc aaa tct ctg caa gtg ttc aga aaa atg ctg act 573
73 Gln Glu Gly Asn Ser Lys Ser Leu Gln Val Phe Arg Lys Met Leu Thr
74 100 105 110 115
76 cct agg ata gag tta tca gtc tgg aaa gat gac ctc acc aca cat gct 621
77 Pro Arg Ile Glu Leu Ser Val Trp Lys Asp Asp Leu Thr Thr His Ala
78 120 125 130
80 gtt gat gct gtg gtg aat gca gcc aat gaa gat ctt ctg cat ggg gga 669
81 Val Asp Ala Val Val Asn Ala Ala Asn Glu Asp Leu Leu His Gly Gly
82 135 140 145
84 ggc ctg gcc ctg gcc ctg gta aaa gct ggt gga ttt gaa atc caa gaa 717
85 Gly Leu Ala Leu Ala Leu Val Lys Ala Gly Gly Phe Glu Ile Gln Glu
86 150 155 160
88 gag agc aaa cag ttt gtt gcc aga tat ggt aaa gtg tca gct ggt gag 765
89 Glu Ser Lys Gln Phe Val Ala Arg Tyr Gly Lys Val Ser Ala Gly Glu
90 165 170 175
92 ata gct gtc acg gga gca ggg agg ctt ccc tgc aaa cag atc atc cat 813
93 Ile Ala Val Thr Gly Ala Gly Arg Leu Pro Cys Lys Gln Ile Ile His
94 180 185 190 195
96 gct gtt ggg cct cgg tgg atg gaa tgg gat aaa cag gga tgt act gga 861
97 Ala Val Gly Pro Arg Trp Met Glu Trp Asp Lys Gln Gly Cys Thr Gly
98 200 205 210
100 aag ctg cag agg gcc att gta agt att ctg aat tat gtc atc tat aaa 909
101 Lys Leu Gln Arg Ala Ile Val Ser Ile Leu Asn Tyr Val Ile Tyr Lys
102 215 220 225
104 aat act cac att aag aca gta gca att cca gcc ttg agc tct ggg att 957
105 Asn Thr His Ile Lys Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile
106 230 235 240
108 ttt cag ttc cct ctg aat ttg tgt aca aag act att gta gag act atc 1005
109 Phe Gln Phe Pro Leu Asn Leu Cys Thr Lys Thr Ile Val Glu Thr Ile
110 245 250 255
112 cgg gtt agt ttg caa ggg aag cca atg atg agt aat ttg aaa gaa att 1053
113 Arg Val Ser Leu Gln Gly Lys Pro Met Met Ser Asn Leu Lys Glu Ile
114 260 265 270 275
116 cac ctg gtg agc aat gag gac cct act gtt gct gcc ttt aaa gct gct 1101
117 His Leu Val Ser Asn Glu Asp Pro Thr Val Ala Ala Phe Lys Ala Ala
118 280 285 290
120 tca gaa ttc atc cta ggg aag agt gag ctg gga caa gaa acc acc cct 1149
121 Ser Glu Phe Ile Leu Gly Lys Ser Glu Leu Gly Gln Glu Thr Thr Pro
122 295 300 305
124 tct ttc aat gca atg gtc gtg aac aac ctg acc ctc cag att gtc cag 1197
125 Ser Phe Asn Ala Met Val Val Asn Asn Leu Thr Leu Gln Ile Val Gln
126 310 315 320
128 ggc cac att gaa tgg cag acg gca gat gta att gtt aat tct gta aac 1245
129 Gly His Ile Glu Trp Gln Thr Ala Asp Val Ile Val Asn Ser Val Asn
130 325 330 335
132 cca cat gat att aca gtt gga cct gtg gca aag tca att cta caa caa 1293
133 Pro His Asp Ile Thr Val Gly Pro Val Ala Lys Ser Ile Leu Gln Gln
134 340 345 350 355
136 gca gga gtt gaa atg aaa tcg gaa ttt ctt gcc aca aag gct aaa cag 1341

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137 Ala Gly Val Glu Met Lys Ser Glu Phe Leu Ala Thr Lys Ala Lys Gln
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140 ttt caa cgg tcc cag ttg gta ctg gtc aca aaa gga ttt aac ttg ttc 1389
141 Phe Gln Arg Ser Gln Leu Val Leu Val Thr Lys Gly Phe Asn Leu Phe
142          375          380          385
144 tgt aaa tat ata tac cat gta ctg tgg cat tca gaa ttt cct aaa cct 1437
145 Cys Lys Tyr Ile Tyr His Val Leu Trp His Ser Glu Phe Pro Lys Pro
146          390          395          400
148 cag ata tta aaa cat gca atg aag gag tgt ttg gaa aaa tgc att gag 1485
149 Gln Ile Leu Lys His Ala Met Lys Glu Cys Leu Glu Lys Cys Ile Glu
150          405          410          415
152 caa aat ata act tcc att tcc ttt cct gcc ctt ggg act gga aac atg 1533
153 Gln Asn Ile Thr Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Asn Met
154 420          425          430          435
156 gaa ata aag aag gaa aca gca gca gag att ttg ttt gat gaa gtt tta 1581
157 Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp Glu Val Leu
158          440          445          450
160 aca ttt gcc aaa gac cat gta aaa cac cag tta act gta aaa ttt gtg 1629
161 Thr Phe Ala Lys Asp His Val Lys His Gln Leu Thr Val Lys Phe Val
162          455          460          465
164 atc ttt cca aca gat ttg gag ata tat aag gct ttc agt tct gaa atg 1677
165 Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser Ser Glu Met
166          470          475          480
168 gca aag agg tcc aag atg ctg agt ttg aac aat tac agt gtc ccc cag 1725
169 Ala Lys Arg Ser Lys Met Leu Ser Leu Asn Asn Tyr Ser Val Pro Gln
170          485          490          495
172 tca acc aga gag gag aaa aga gaa aat ggg ctt gaa gct aga tct cct 1773
173 Ser Thr Arg Glu Glu Lys Arg Glu Asn Gly Leu Glu Ala Arg Ser Pro
174 500          505          510          515
176 gcc atc aat ctg atg gga ttc aac gtg gaa gag atg tat gag gcc cac 1821
177 Ala Ile Asn Leu Met Gly Phe Asn Val Glu Glu Met Tyr Glu Ala His
178          520          525          530
180 gca tgg atc caa aga atc ctg agt ctc cag aac cac cac atc att gag 1869
181 Ala Trp Ile Gln Arg Ile Leu Ser Leu Gln Asn His His Ile Ile Glu
182          535          540          545
184 aat aat cat att ctg tac ctt ggg aga aag gaa cat gac att ttg tct 1917
185 Asn Asn His Ile Leu Tyr Leu Gly Arg Lys Glu His Asp Ile Leu Ser
186          550          555          560
188 cag ctt cag aaa act tca agt gtc tcc atc aca gaa att atc agc cca 1965
189 Gln Leu Gln Lys Thr Ser Ser Val Ser Ile Thr Glu Ile Ile Ser Pro
190          565          570          575
192 gga agg aca gag tta gag att gaa gga gcc cgg gct gac ctc att gag 2013
193 Gly Arg Thr Glu Leu Glu Ile Glu Gly Ala Arg Ala Asp Leu Ile Glu
194 580          585          590          595
196 gtg gtt atg aac att gaa gat atg ctt tgt aaa gta cag gag gaa atg 2061
197 Val Val Met Asn Ile Glu Asp Met Leu Cys Lys Val Gln Glu Glu Met
198          600          605          610
200 gca agg aaa aag gag cga ggc ctt tgg cgc tcg tta gga cag tgg act 2109
201 Ala Arg Lys Lys Glu Arg Gly Leu Trp Arg Ser Leu Gly Gln Trp Thr

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202          615          620          625
204 att cag caa caa aaa acc caa gac gaa atg aaa gaa aat atc ata ttt 2157
205 Ile Gln Gln Gln Lys Thr Gln Asp Glu Met Lys Glu Asn Ile Ile Phe
206          630          635          640
208 ctg aaa tgt cct gtg cct cca act caa gag ctt cta gat caa aag aaa 2205
209 Leu Lys Cys Pro Val Pro Pro Thr Gln Glu Leu Leu Asp Gln Lys Lys
210          645          650          655
212 cag ttt gaa aaa tgt ggt ttg cag gtt cta aag gtg gag aag ata gac 2253
213 Gln Phe Glu Lys Cys Gly Leu Gln Val Leu Lys Val Glu Lys Ile Asp
214 660          665          670          675
216 aat gag gtc ctt atg gct gcc ttt caa aga aag aag aaa atg atg gaa 2301
217 Asn Glu Val Leu Met Ala Ala Phe Gln Arg Lys Lys Lys Met Met Glu
218          680          685          690
220 gaa aaa ctg cac agg caa cct gtg agc cat agg ctg ttt cag caa gtc 2349
221 Glu Lys Leu His Arg Gln Pro Val Ser His Arg Leu Phe Gln Gln Val
222          695          700          705
224 cca tac cag ttc tgc aat gtg gta tgc aga gtt ggc ttt caa aga atg 2397
225 Pro Tyr Gln Phe Cys Asn Val Val Cys Arg Val Gly Phe Gln Arg Met
226          710          715          720
228 tac tcg aca cct tgc gat cca aaa tac gga gct ggc ata tac ttc acc 2445
229 Tyr Ser Thr Pro Cys Asp Pro Lys Tyr Gly Ala Gly Ile Tyr Phe Thr
230          725          730          735
232 aag aac ctc aaa aac ctg gca gag aag gcc aag aaa atc tct gct gca 2493
233 Lys Asn Leu Lys Asn Leu Ala Glu Lys Ala Lys Lys Ile Ser Ala Ala
234 740          745          750          755
236 gat aag ctg atc tat gtg ttt gag gct gaa gta ctc aca ggc ttc ttc 2541
237 Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly Phe Phe
238          760          765          770
240 tgc cag gga cat ccg tta aat att gtt occ cca cca ctg agt cct gga 2589
241 Cys Gln Gly His Pro Leu Asn Ile Val Pro Pro Pro Leu Ser Pro Gly
242          775          780          785
244 gct ata gat ggt cat gac agt gtg gtt gac aat gtc tcc agc cct gaa 2637
245 Ala Ile Asp Gly His Asp Ser Val Val Asp Asn Val Ser Ser Pro Glu
246          790          795          800
248 acc ttt gtt att ttt agt ggc atg cag gct ata cct cag tat ttg tgg 2685
249 Thr Phe Val Ile Phe Ser Gly Met Gln Ala Ile Pro Gln Tyr Leu Trp
250          805          810          815
252 aca tgc acc cag gaa tat gta cag tca caa gat tac tca tca gga cca 2733
253 Thr Cys Thr Gln Glu Tyr Val Gln Ser Gln Asp Tyr Ser Ser Gly Pro
254 820          825          830          835
256 atg aga ccc ttt gca cag cat cct tgg agg gga ttc gca agt ggc agc 2781
257 Met Arg Pro Phe Ala Gln His Pro Trp Arg Gly Phe Ala Ser Gly Ser
258          840          845          850
260 cct gtt gat taatctctac atcatttttaa cagctggtat ggccttacct 2830
261 Pro Val Asp
263 tgggtgaact aaocaaataa tgaccatcga tggctcaaag agtggcttga atatatccca 2890
265 tgggttatct gtatggactg actgggttat tgaaaggact agccacatac tagcatctta 2950
267 gtgcctttat ctgtctttat gtcttggggg tggggtaggt agataccaaa tgaaacactt 3010
269 tcaggacett ccttctctct gcagttgttc tttaatctcc tttactagag gagataaata 3070

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TIME: 14:11:04

Input Set : A:\SEQLIST.txt

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273 gatgatagta taaaaatggt aggataacag aatgatttta gattttccag agaataattat 3190
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288 20 25 30
290 Ile Phe Pro Gln Trp Arg Lys Gly Asn Thr Glu Glu Cys Leu Pro Tyr
291 35 40 45
293 Lys Cys Ser Glu Thr Gly Ala Leu Gly Glu Asn Tyr Ser Trp Gln Ile
294 50 55 60
296 Pro Ile Asn His Asn Asp Phe Lys Ile Leu Lys Asn Asn Glu Arg Gln
297 65 70 75 80
299 Leu Cys Glu Val Leu Gln Asn Lys Phe Gly Cys Ile Ser Thr Leu Val
300 85 90 95
302 Ser Pro Val Gln Glu Gly Asn Ser Lys Ser Leu Gln Val Phe Arg Lys
303 100 105 110
305 Met Leu Thr Pro Arg Ile Glu Leu Ser Val Trp Lys Asp Asp Leu Thr
306 115 120 125
308 Thr His Ala Val Asp Ala Val Val Asn Ala Ala Asn Glu Asp Leu Leu
309 130 135 140
311 His Gly Gly Gly Leu Ala Leu Ala Leu Val Lys Ala Gly Gly Phe Glu
312 145 150 155 160
314 Ile Gln Glu Glu Ser Lys Gln Phe Val Ala Arg Tyr Gly Lys Val Ser
315 165 170 175
317 Ala Gly Glu Ile Ala Val Thr Gly Ala Gly Arg Leu Pro Cys Lys Gln
318 180 185 190
320 Ile Ile His Ala Val Gly Pro Arg Trp Met Glu Trp Asp Lys Gln Gly
321 195 200 205
323 Cys Thr Gly Lys Leu Gln Arg Ala Ile Val Ser Ile Leu Asn Tyr Val
324 210 215 220
326 Ile Tyr Lys Asn Thr His Ile Lys Thr Val Ala Ile Pro Ala Leu Ser
327 225 230 235 240
329 Ser Gly Ile Phe Gln Phe Pro Leu Asn Leu Cys Thr Lys Thr Ile Val
330 245 250 255
332 Glu Thr Ile Arg Val Ser Leu Gln Gly Lys Pro Met Met Ser Asn Leu
333 260 265 270
335 Lys Glu Ile His Leu Val Ser Asn Glu Asp Pro Thr Val Ala Ala Phe
336 275 280 285
338 Lys Ala Ala Ser Glu Phe Ile Leu Gly Lys Ser Glu Leu Gly Gln Glu
339 290 295 300
341 Thr Thr Pro Ser Phe Asn Ala Met Val Val Asn Asn Leu Thr Leu Gln
342 305 310 315 320
344 Ile Val Gln Gly His Ile Glu Trp Gln Thr Ala Asp Val Ile Val Asn

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,762

DATE: 11/14/2001

TIME: 14:11:05

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF3\11142001\I830762.raw

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